NCBI   Blast 2 Sequences results

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]

Matrix BLOSUM62 ▾ gap open: 11   gap extension: 1
x_dropoff: 50   expect: 10.000 wordsize: 3   Filter ☑ View option Standard ▾
Masking character option X for protein, n for nucleotide ▾   Masking color option Black ▾
☐ Show CDS translation   Align

Sequence 1: gi|47117817|sp|O75376|NCOR1_HUMANNuclear receptor corepressor 1 (N-CoR1) (N-CoR).
Length = 312 (1 .. 312)   SEQ ID NO: 11

Sequence 2: gi|4559296|gb|AAD22972.1|AF125671_1silencing mediator of retinoic acid and thyroid hormone receptor extended isoform [Mus musculus]
Length = 2462 (1 .. 2462)
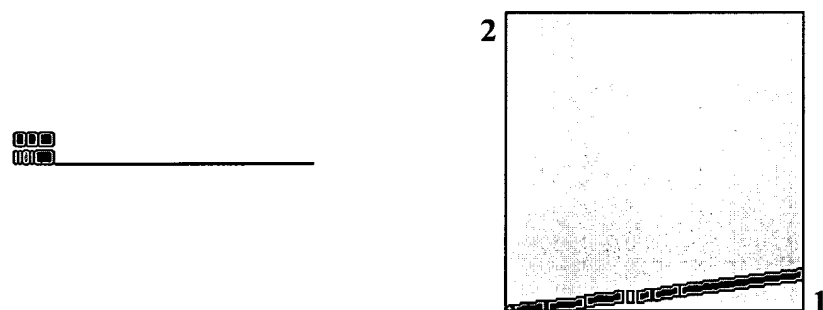
NOTE:Bitscore and expect value are calculated based on the size of the nr database.

```
 Score =  200 bits (508),  Expect = 1e-49
 Identities = 179/315 (56%),  Positives = 204/315 (64%),  Gaps = 14/315 (4%)

Query  1    MSSSGYPPNQGAFSTEQSRYPPHSVQYTFPNTRHQQEFAVPDYRSSHLEVXXXXXXXXXX  60
            MS S  P  Q  +   + RYPPH + Y    R   +  + +Y+  H    S L
Sbjct  1    MSGSTQPVAQ-TWRAAEPRYPPHGISYPVQIARSHTDVGLLEYQ--HHPRDYTSHLSPGS  57

Query  61   XXXXXXXXXXXXXXEFHPGSDRPQER--RTSYEPFHPGPSPVDHDSLESKRPRLEQVSDSH  118
                Q  RRRPSLLSEF PGS+R QE   R     F P    D +  ESKRPRLE + D+
Sbjct  58   IIQPQRRRPSLLSEFQPGSERSQELHLRPESRTFLPELGKPDIEFTESKRPRLELLPDTL  117

Query  119  FQRVSAAVLPLVHPLPEGLRASADAKKDPAFGGKHEAPSSPISGQPCGDDQNASPSKLSK  178
            +      L   P G   S D  KD + GK E P SP S       +   +PS+LSK
Sbjct  118  LRPSPL----LATGQPSG---SEDLTKDRSLAGKLE-PVSPPSPPHADPELELAPSRLSK  169

Query  179  EELIQS-MDRVDREIAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXHRSIVQ  237
```

```
                EELIQ+ +DRVDREI   VEQQI KLKKKQQQLEEEAAKPPEPEKPVSPPP+E KHRS+VQ
Sbjct   170     EELIQNRLDRVDREITMVEQQISKLKKKQQQLEEEAAKPPEPEKPVSPPPIESKHRSLVQ   229

Query   238     IIYDENRKKAEEAHKIFEGLGPKVELPLYNQPSDTKVYHENIKTNQVMRKKLILFFKRRN   297
                IIYDENRKKAE AH+I EGLGP+VELPLYNQPSDT+ YHENIK NQ MRKKLIL+FKRRN
Sbjct   230     IIYDENRKKAEAAHRILEGLGPQVELPLYNQPSDTRQYHENIKINQAMRKKLILYFKRRN   289

Query   298     HARKQREQKICQRYD   312
                HARKQ EQ+ CQRYD
Sbjct   290     HARKQWEQRFCQRYD   304
```

```
CPU time:     0.04 user secs.        0.02 sys. secs          0.06 total secs.

Lambda       K        H
   0.314     0.131     0.385

Gapped
Lambda       K        H
   0.267    0.0410     0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 5554
Number of extensions: 3510
Number of successful extensions: 5
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 312
Length of database: 1,199,905,207
Length adjustment: 132
Effective length of query: 180
Effective length of database: 1,199,905,075
Effective search space: 215982913500
Effective search space used: 215982913500
Neighboring words threshold: 9
X1: 16 ( 7.2 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 42 (21.9 bits)
S2: 78 (34.7 bits)
```